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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Biochemistry, Chinese Academy of
Shanghai 200031, P.R. China
Location/Qualifiers
                       4 (515b1s 4 (bases 38597 to 38672)
A (bases 38597 to 38672)
Dahlberg, J. E. and Blattner, F. R.
In vitro transcription products of lambda DNA and regulatory sites
(in) Fox, C. F. and Robinson, W. S. (Eds.);
(in) Fox, C. F. and Robinson, W. S. (Eds.);
(in) POX, C. F. and Robinson, W. S. (Eds.);
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Bacteriophage lambda, complete genome.
702459 M17233 M24325 V00636 X00906
J02459.1 GI:215104
DNA-Dindian
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Bacteriophage lambda
Bacteriophage lambda
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
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4931680
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Imada.M. and Tsugita.A.
Amino acid sequence of lambda phage endolysin
Nature New Biol. 233, 230-231 (1971)
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3'-terminal nucleotide sequences of bacteriophage lambda
rensel. Acad. Sci. U.S.A. 70 (4), 1151-1155 (1973)
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VHLSSYVEVIFIGLSSSERRSLICFENYETVIVILLAYNDLITAVYRDIVFLIYKVD
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HATVANDLFRNMLASYXFECKNSEPHIKSIRSLPISVYISTFIIFMIPRKNLFSLLAR
HATVANDLFRNMLASYXFECKNSEPHIKSIRSLPISVYISTFIIFMIPRKNLFSLLAR
IQYSEPHIGKSFKSIIGFRFASINSDCSCRKRCGRTIFFYNFYERVSLSNHFTQVLPC
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bacteriophage lambda
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Walz, A., Pirrotta, V. and I
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Mucleotide sequence of the rightward operator of phage
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Davies, R.W., Schreier, P.H. a
Nucleotide sequence of the a
Nature 270 (5639), 757-760 (
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Nature 272 (5652), 414-423 (1978)
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Denniston-Thompson,K., Moore,D.D., Kruger,K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                   24 (bases 37990 to 38982)
Schwarz, E., Scherer, G., Hobom, G. and Kossel,
Nucleotide sequence of cro, cII and part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutational analysis of the operators of bacteriophage Mol. Gen. Genet. 166 (1), 61-73 (1978) 79114073
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                                                                                                   DNA sequence of the bacteriophage Nature 276 (5685), 301-302 (1978)
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    Nucleotide sequence of the O
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barten, B., Linton, L., Nusbaum, C., Bastlen, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Anderson, S., Baldwin, J., Brown, A., Burkett, G., Boguslavkly, L., Bokhgalter, B., Brown, A., Burkett, G., Boguslavkly, L., Bokhgalter, B., Brown, A., Burkett, G., Collymore, A., Costle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dondino, M., Doyle, M., Ferreitra, P., Fitzugh, W., Gage, D., Dodge, S., Domino, M., Doyle, M., Ferreitra, P., Fitzugh, W., Gage, D., Collymore, R., Jan, L., Graham, L., Galagan, J., Graham, L., Galagan, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lanazares, R., Landers, T., Lehoczky, J., Klein, J., LaRocque, K., Lanazares, R., Landers, T., McGurk, A., McKernan, K., McPheeters, R., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGurt, A., McGurk, A., McKernan, K., McPheeters, R., McGurt, A., McGurk, A., McGurt, A., McG
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Birren, B., Linton, L., Nusbaum, C
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Davies, R.W., Schreder, P.H. and Buchel, D.E.
Determination of the endpoints of partial deletion mutants of
attachment site of bacteriophage lambda by DNA sequencing
Nucleic Acids Res. 5 (9), 3209-3218 (1978)
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Nucleic Acids Res. 5 (9), 3141-3156 (1978)
79033241
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Homo sapiens chromosome 18 clone RP11-286N3
SEQUENCE, 26 unordered pieces.
AC069496
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Hoess,R.H. and Landy,A.
Structure of the lambda att
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            Submitted (01-JUN-2000) whitehead Institute/MIT Center for Submitted (01-JUN-2000) whitehead Institute/MIT Center for Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Robert 1, 2000 this sequence version replaced 91:8141034. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Length 48502;

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http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
center: Whitehead Institute/ MIT Center for Genome Research
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ing draft' sequence. It cur
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
AL published Only in Database (2002)
22 (bases 1 to 213005)
22 (bases 1 to 213005)
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24 (bases 1 to 213005)
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Homo sapiens genomic DNA, chromosome 18 clone:RPI1-286N3, complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 188199)
Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Dietrich, N.L., Eagle, W.O., Gupta, J., Ho, S.~L.,
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188199 bp
Mus musculus chromosome 13 clone
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ACU79247
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mus musculus
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Idol,J., Lee-Lin,S.-Q., Legaspi,R., Lim,M., Maduro, Maduro, V.B., Mastrian,S.D., McCloskey,J.C., McDowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 178114 bases at least Q40
Consensus quality: 182587 bases at least Q20
Consensus quality: 182587 bases at least Q20
Consensus quality: 182587 bases at least Q20
Insert size: 187000; agarose-fp
Insert size: 191000; pulse-field-gel
Insert size: 191000; pulse-field-gel
Quality coverage: 4.77x in Q20 bases; pulse-field-gel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: nisc_mouseenbgri.nih.
------ Project Information
Center project name: ts
Center clone name: 475C06
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23620
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47731
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577235
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gap of unknown length contig of 9604 bp in le gap of unknown length contig of 12011 bp in 1 gap of unknown length contig of 6767 bp in length contig of 6767 bp in length contig of 11119 bp in 1
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gap of unknown length
contig of 2560 bp in length
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of 3250
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|152408 GCAACAGTGGCATGCAC 152392
                                                                                                      ch 77.3%; Score 17; DB 2; Similarity 100.0%; Pred. No. 3.9; 17; Conservative 0; Mismatches
                                                                                                                                                                            54769
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/clone_lib="RPCI mouse BAC library 23"
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ol_type="genomic DNA"
train="C57BL6/J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="assembly_fragment"
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Baylor Plaza, Houston, TX 77030, USA
on Nov 23, 2002 this sequence version replaced g1:24417979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 8 contigs. The true order of the pleces
is not known and their order in this sequence record is
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
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Center clone name: KCRL

Center clone name: KCRL

Center clone name: CH300-431M13

Center clone name: CH300-431M13

Center clone name: CH300-431M13

Center clone name: Phrap; version 0.990329

Assembly program: Phrap; version 0.990329

Consensus quality: 165059 bases at least Q40

Consensus quality: 165059 bases at least Q30

Consensus quality: 165050 bases at least Q30

Consensus quality: 165050 bases at least Q30

Consensus quality: 165050 bases; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                          /note="wgs_contig"
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/mol.type="genomic DNA"
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164563. .165629
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4018: gap of unknown length
164462: contig of 160444 bp in length
164562: gap of unknown length
180515: contig of 15953 bp in length
180615: gap of unknown length
181914: contig of 1299 bp in length
182034: contig of 1219 bp in length
182034: contig of 1219 bp in length
183333: gap of unknown length
183333: gap of unknown length
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISSPROT; Tr:, TREMBL:
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Query Match
Best Local
      Score 17;
Pred. No.
Mismatches
0;
              Length 188593;
  0;
  Gaps
  0;
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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 204453)
                                                                                                                                                                                                                                                                                                AL596324 204453 bp DNA linear ROD 14-MAR-2002
Mouse DNA sequence from clone RP23-324M14 on chromosome 11,
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AL Submitted (14 MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
humquery@sanger.ac.uk Clone request@sanger.ac.uk
humquery@sanger.ac.uk
clone request@sanger.ac.uk
request@san

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-324M14 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

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180394. 180404.
/note-"Sequence from uni-directional dGTP big dye terminator reads only."
48080 c 47102 g 58827 t

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Consensus quality: 2008873 bases at least 020
Consensus quality: 210606 bases at least 020
Consensus quality: 210606 bases at least 020
Consensus quality: 210606 bases at least 020
Estimated insert size: 185170; agarose-fp estimation
Estimated insert size: 214034; sum-of-contigs estimation
Quality coverage: 8.54 in 020 bases; sum-of-contigs estimation
Quality coverage: 7.48 in 020 bases; sum-of-contigs estimation
**NOTE: This is a 'working draft' sequence. It currently
** consists of 18 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
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1 Similarity 100.0%;
17; Conservative (
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DOE Joint Genome Institute.
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HTG; HTGS_PHASE1; HTGS_DRAFT:
MUS mUSCULUS (house mouse)
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Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Center Project Name: 1809981
Center clone name: RPCI-23_190G5
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.jgi.doe.gov
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1475: gap of .
2675: contig
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HTG: HTGS_PHASE1; HTGS_DRAFT.
Atelerix albiventris (middle-African hedgehog)
Atelerix albiventris
Eukaryota; Metazoa; Chordata; Craniata; Verteb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC131892 220618 bp DNA linear Atelerix albiventris clone LB4-341F7, WORKING DRAFT
                                                                                                         Submitted (27-AGG-2002) Genome Sciences, L
Laboratory, 1 Cyclotron Rd., Berkeley, CA
Draft Sequence Produced by Berkeley PGA
Web site: http://pga.lbl.gov
Center Code: PGABERK
Center Code: PGABERK
Center PGOJECT Name: E011-341P7
Bac Clone Name: LB4-341P7
                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 220618)
Martin, J., Schwartz, J.R., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M.
and Cheng, J. F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unordered pieces.
                                                                                                                                                                                                                                                             2 (bases 1 to 220618)
Martin,J., Schwartz,J.R., Hosseini,R., Peng,Y., Peng,Z., Rubin,E.M.
and Cheng,J.<sup>-F</sup>.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae;
available at:
http://ppa.lbl.gov/cgi-bin/search_cvcgd?type=n&value=PLG
http://ppa.lbl.gov/cgi-bin/search_cvcgd?type=n&value=PLG
fundling agent: Programs for Genomic Applications (NHLBI)
contact: 'Jody Schwartz' jrschwartz@lbl.gov
                                                                                                                                                                                                                                                 Direct Submission
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                                                                       Additional information on comparative analysis and ordering
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ilarity 100.0%;
Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-19065"
/clone="RPCI mouse BAC library 23"
/clone_lib="RPCI mouse BAC library 23"
/clone_11b="RPCI mouse BAC library 23"
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5346: gap of unknown length
67573: contrig of 14133 bp in 1
67673: gap of unknown length
167673: gap of unknown length
186447: gap of unknown length
110834: contrig of 24387 bp in 1
110934: gap of unknown length
110934: gap of unknown length
148079: contrig of 37145 bp in 1
148079: gap of unknown length
148179: gap of unknown length
148179: gap of for555 bp in 1
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A 94720, USA
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SEQUENCE, 24
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* NOTE: This is a "vorking draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid; pUC18
Chemistry: Dye-terminator Big Dye
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for a description: http://www-gsd.lbl.gov/cheng/BAC.html
ch 77.3%; Score 17; DB 2; Length 220618; l Similarity 100.0%; Pred. No. 3.8; 17; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                        57797
                                                                                                                                                                                                                         /organism="Atelerix albiventris"
/mol_type="genomic DNA"
/db_xref="taxon:9368"
                                                                                                                                                             /clone="LB4-341P7"
49736 c 49846 g 60939 t
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0618: contig of 7778
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171608 CAACAGTGGCATGCACC 171624
                                                                                                                               RES MIZEN, D. MATIE., METAKEN, Lee., ADTAMZON, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Barber, H., Bars, B., Allen, H., Allen,
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AC120469.5 GI:25090406
HTG; HTGS_PHASE1; HTGS_FULLTOP
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Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
               2 (bases 1 to 226286) Worley, K.C.
                                                                              Unpublished
                                                                                                                        Submission
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FEATURES source

BASE COUNT ORIGIN

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AUTHORS
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Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced 91:23265457.
On Nov 19, 2002 this sequence version replaced 91:23265457.
On How 19, 2002 this assembly is a combination of BAC based reads and whole genome shortun sequencing reads assembled using Atlas and whole genome shortun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas in the genence contigs are ordered and oriented, and separated individual sequence contigs are ordered and oriented, and separated individual sequence contigs are ordered and there may be sequence by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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Submitted (07-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Subases 1 to 226286)
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Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: GMXN
Center clone name: CH230-209C24
Center clone name: CH230-209C24
Center clone name: CH230-209C24
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Center clone clone close close
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the places is not known and their order in this sequence record is is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will he preserved.
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/note="clone_boundary
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225087: gap of unknown length
226286: contig of 1199 bp in length.
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RS Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anglano, D., Allen, H., Alsbrooks, S., Amin, A., Anglano, D., Allen, H., Alsbrooks, S., Amin, A., Anglano, D., Anglano, D., Anglano, D., Bander, M., Banster, M., Barster, M., Barster, M., Banster, M., Barster, M., Barster, M., Barster, M., Calderon, E., Balada, M., Calderon, M., Calderon, M., Buster, M., Canderon, M., Buster, M., Canderon, M., Buster, M., Canderon, M., Buster, M., Canderon, M., Buster, M., Davala, M., Durbin, K., Duval, B., Zaves, K., Davala, M., Davala, M., Duvala, B., Daves, K., Paga, M., Barster, M., Foster, M., Foster, M., Farster, C.M., Gabisla, M., Garcia, A., Garner, T., Garza, M., Farster, K., Galtz, M., Garza, M., Gebregocyis, E., Gebre, K., Gill, R., Gardia, A., Garner, M., Guerra, M., Gunarathe, P., Haaland, M., Hamilton, K., Garza, M., Gebregocyis, B., Goster, K., Galtz, M., Garza, M., Gebregocyis, B., Howells, S., Hulyk, S., Hune, J., Johnson, R., Liz, J., Kally, S., Kally, S., Khan, Z., Kally, L., Kovis, C., Karati, C., Luly, J., Louda, H., Johnson, R., Johnson,
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Rattus norvegicus (Norway rat)
Rattus norvegicus (Phordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus clone CH230-315111, WORKING DRAFT SEQUENCE, 2
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66689 a 42172 c 42775 g 64932 t
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Direct Submission

Direct Submission

Submitted (20 Nov-2002) Human Genome Sequencing Center, Department

Submitted (20 Nov-2002) Human Genetics, Baylor College of Medicine, One

of Molecular and Human Genetics, USA

Baylor plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:24181992.

On Nov 20, 2002 this sequencing reads assembled using Atlas

and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

in the feature table below represents a scaffold in the Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described

in the feature table below represents a scaffold in the Atlas

in the feature table below represents a scaffold in the Atlas

individual sequence contigs are ordered and oriented, and separated

by sized gaps filled with Ns to the estimated size. The sequence

by sized gaps filled with Ns to the clone and there may be sequence

may extend beyond the ends of the clone and there may be sequence

may extend beyond the ends of the clone and there may be sequence

shotgun sequence reads. Both end sequences and whole genome

shotgun sequence conly contigs will be indicated in the feature
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Rat Genome Sequencing Consortium
Direct Submission
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center clone name: CR20
Center clone name: CH230-31511
Center clone name: CH230-31511
Center project name: Phrap; version 0.990329
Consensus quality: 195238 bases at least 030
Consensus quality: 197819 bases at least 030
Consensus quality: 197819 bases at least 030
Consensus quality: 199492 bases at least 030
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ch 77.3%; Score 17; DB 2; Similarity 100.0%; Pred. No. 3.8; 17; Conservative 0; Mismatches
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pleces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the filished sequence
as soon as it is available and the accession number will
be preserved.
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4 234120: contig of 6887 bp in length.
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15010 GGCAACAGTGGCATGCA 15026
                                                                                                                                                                                                                               NESS I (D. 224.42)

MILED, C. Marie, Metzker M. Lee, Abranzon, S. Adams, C. Alder, J. Allien, G. Allien, H. Alsbrooks, S. Amin, A. Angeliano, D. Allien, G. Allien, H. Alsbrooks, S. Amin, A. Angeliano, D. Allien, G. Allien, H. Alsbrooks, S. Amin, A. Angeliano, D. Angeliano, D. Allien, G. Allien, H. Angeliano, A. Aydeliano, B. Barderian, C. Chen, Z. Chu, J. Chacko, J. Chacko, J. Chacko, J. Chacko, J. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chen, C. Coxie, M. Gree, A. D'Souza, L. Chacko, J. Chen, J. Liu, J. Liu, W. J. Liu, J. Liu, W. J. Liu, J. Liu, W. J. Liu, J. Liu, J. Liu, W. J. London, J. Longacre, S. Lopez, J. Liu, J. Liu, W. J. Karpathy, S. Kelty, S. Khan, J. Levan, J. Liu, J. Liu, W. J. Kelly, S. Mancuen, J. Liu, J. Karpathy, S. Kelty, S. Mancuen, J. Liu, J. Liu, J. Liu, J. Liu, W. J. Liu, J. 
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AC133845.3 GI:30522110
AC133845.3 GI:30522110
HTG; HTGS_PHASEI; HTGS_ENRICHED.
HTG; HTGS_PHASEI; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus (Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC133845 234325 bp 1
Rattus norvegicus clone CH230-41J2,
                                                                                                                                                                                                                          and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA linear HTG 10-MAY-2003
, *** SEQUENCING IN PROGRESS ***,
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SEQUENCE,

linear HTG 27-SEP-2002 E, 5 ordered pieces.

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REFERENCE
AUTHORS
TITLE
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BASE COUNT.
ORIGIN
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On May 10, 2003 this sequence version replaced gi:25013050.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/Tat/). Bach contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold indyridual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat Genome Sequencing Consortium.
Direct Submission
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Submitted (19-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 234325)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces.

* is not known and their order in this sequence record is

* arbitrary Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* this record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: project name: GEVF
Center clone name: CH200-441/2
Center clone name: CH200-441/2
Center clone name: CH200-441/2
Center clone name: CH200-441/2
Consensus quality: 226523 bases at least Q40
Consensus quality: 226523 bases at least Q20
Consensus quality: 227917 bases at least Q20
Estimated insert size: 237878; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor Co
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                                                                                                                                                           end_sequence:BH342505"
complement(230261. .23
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/mol_type="genomic INA"
/db_xref="taxon:10116"
/clone="CH230-41J2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location
                                                                                                                                                                                                                                                                                                                               note="clone_boundary"
                               d_sequence:BH342503"
46115 c 45629 g 69420 t
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                                                                                                                                                                                                                                                                                                                                                           wgs_end_extension
ind:Sp6"
53657
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AC134520/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: plasmid; pUC18
Chemistry: Dye-terminator Big Dye
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329
Assembly program: Phrap version 0.990329
This sequence is the joint assembly of the overlapping clones
This sequence is the joint assembly of the overlapping clones
This 1s a that-341P7. Nucleotides 169179-237739 overlap with
Nucleotides 1-70766 of clone LB4-390B15 (AC122114).
** NOTE: This is a 'vorking draft' sequence. It currently
** consists of 5 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
** to the gaps between them are based on estimates that have
** provided by the submittor.
** This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GGCAACAGTGGCATGCA 19
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Martin, J., Schwartz, J.R., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and Cheng, J.-F.
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Atelerix albiventris (middle-African hedgehog)
Atelerix albiventris
Atelerix albiventris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Erinaceidae; Erinaceinae;
Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae;
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AC134520.1 GI:23334716
HTG; HTGS_PHASE2; HTGS_I
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Atelerix albiventris, WORKING DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           available at:
http://pgq.lbl.gov/cgi-bin/search_cvcgd?type=n&value=
http://pgq.lbl.gov/cgi-bin/search_cvcgd?type=n&value=
Funding agent: Programs for Genomic Applications (NHLBI)
Contact: 'Jody Schwartz' jrschwartz@lbl.gov
Summary Statistics:
Summary Statistics:
Summary Statistics:
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Bac Clone Name:joint assembly of clones LB4-253J19 and LB4-341P7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://pga.lbl.gov
Center Code: PGABERK
Center Project Name: E010_E0
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Martin,J., Schwartz,J.R., Hosseini,R., Peng,Y., Peng,Z., Rubin,E.M.
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Submitted (27-SEP-2002) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
                                                                                                               This sequence will be replaced

This sequence will be replaced
by the finished sequence as soon as it is available and
by the finished sequence as soon as it is available and
the accession number will be preserved.

156241: contig of 56241 bp in length
156342: 131145: contig of 74804 bp in length
131146: 131245: gap of unknown length
131246: 131245: gap of unknown length
142561: 142560: contig of 13135 bp in length
142661: 142660: gap of unknown length
142661: 173976: contig of 31316 bp in length
173977: 14076: gap of unknown length
173977: 237739: contig of 63663 bp in length.
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               /organism-"Atelerix albiventris"
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Matches 17
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Sequencing vector: plasmid, 100%
Sequencing vector: plasmid, 100%
Sequencing vector: plasmid, 100%
Sequencing vector: plasmid, 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 2526176 bases at least 030
Consensus quality: 251676 bases at least 030
Consensus quality: 25260 bases at least 020
Insert size: 232000; agarose-fp
Insert size: 232000; agarose-fp
Quality coverage: B.97 in 020 bases; sum-of-contigs
Quality coverage: B.97 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 77.3%; So 18 similarity 100.0%; 117; Conservative 0;
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AC135085
AC135085 GI:23505660
HTG; HTGS_PHASE1; HTGS_DRAI
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC135085 258520 bp DNA linear HTG 11-OCT-2002 Mus musculus chromosome UNK clone RP24-317P24, WORKING DRAFT SEQUENCE, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 258520)
McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
Project Information
Center project name: M_BB0317P24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site:http://genome.wustl.edu/qsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 258520)
3 (chases 1 to 258520)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (11-0CT-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Sibmitted (05-0CT-2002) Genome Sequencing Center, 4444 Forest Park
Submitted (05-0CT-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 258520) (cherson, J.D. and Waterston, R.H.
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                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be processed.
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HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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/db_xref="taxon:9368"
53997 c 54516 g 64281 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Summary Statistics -----
1120: contig of 1120 bp in length 1220: gap of unknown length
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10000"
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/clone="RP24-317P24"
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/83303 . 106028

/note="assembly_name:Contig45"

106129 . 142804

/note="assembly_name:Contig46"

14205 . 182719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of unknown

of unknown length

contig of 3924 bp 1.

ap of unknown length

contig of 9177 bp in length

contig of 91877 bp in length

i gap of unknown length

i gap of unknown length

js contig of 13044 bp in length

j5 contig of 13044 bp in length

j5 gap of unknown length

f61: contig of 9566 bp in length

f62: gap of unknown length

f63: gap of unknown length

f63: gap of unknown length

f63: contig of 6941 bp in length

f62: contig of 6947 bp in length

f62: contig of 6967 bp in length

f62: gap of unknown length

f63: gap of unknown length

f64: gap of unknown length

f65: gap of unknown length

f66: gap of unknown length

f67: gap o
                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig43" 66262 . 83202
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19678. .28874
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/note="assembly_name:Cont1g38"
15654. .19577
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                                                                                            note-"assembly_name:Contig47"
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te-"assembly_name:Contig34"
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e="assembly_name:Contig37"
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unknown length
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own length
210 bp in length
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216363 TTGGCAACAGTGGCATG 216347
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                                                                                                                                                                                                                                                        sequencing vector: M13; 0%
sequencing vector: M13; 0%
sequencing vector: plasmid; 100%
sequencing vector: plasmid; 100%
chemistry: Dye-terminator B19 Dye; 100% of reads
chemistry: Dye-terminator B19 Dye; 100%
consensus quality: 256417 bases at least 030
consensus quality: 258611 bases at least 030
consensus quality: 258611 bases at least 020
consensus quality: 258611 bases at least 030
consensus quality: 258611 bases at least 040
consensus quality: 258611 bases at least 030
consensus quality
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2 (Dases 1 to 263181)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (27-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (Dases 1 to 263181)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submisted (11-CCT-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
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AC134608
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McPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
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HTGS_PHASSI; HTGS_DRAFT; HTGS_FULLTOP
MUS "MUSCULUS (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
Project Information
Center project name: M_BA0068H13
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                                                                                                                                                                                                                                          as soon as it
be preserved.
                                            1699: contig of 1699 bp in length
1799: gap of unknown length
3204: contig of 1405 bp in length
3304: gap of unknown length
5390: contig of 2066 bp in length
5490: gap of unknown length
5490: gap of unknown length
7591: contig of 2101 bp in length
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bp in length
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                                                         ch 77.3%; Score 17; DB 2; Length 263181; Similarity 100.0%; Pred. No. 3.7; 17; Conservative 0; Mismatches 0; Indels 0
          4 GCAACAGTGGCATGCAC 20
                                                                                                                                                                                                     79384 a
                                                                                                                                                                                                     /note="assembly_name:Contig30"
/261960 . 263181
/note="assembly_name:Contig7"
53228 c 53271 g 75642 t
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/db_xref="taxon:10090"
/chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                        /note-"assembly_name:Cont1g28"
96775. .170070
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73571. .96674
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9353. .22287
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70171. .261859
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28707: contly of 6320 bp in length
28807: gap of unknown length
39035: contly of 10228 bp in length
39135: gap of unknown length
51322: contly of 12097 bp in length
51332: gap of unknown length
51370: gap of unknown length
73470: contly of 22138 bp in length
73570: gap of unknown length
96744: contly of 23130 bp in length
170070: contly of 73296 bp in length
170070: gap of unknown length
170170: gap of unknown length
170170: gap of unknown length
170170: gap of unknown length
261959: gap of unknown length
261959: gap of unknown length
261959: gap of unknown length
261951: contly of 1222 bp in length
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_7591
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_.28707
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: contig of 2383 bp in length
: gap of unknown length
: contig of 1836 bp in length
: gap of unknown length
: gap of unknown length
contig of 3584 bp in length
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                                                                       Gaps
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Search completed: September 26, 2003, 07:40:29 Job time : 453.617 secs